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OM protein - protein search, using sw model

Run on: December 29, 2005, 15:28:28 ; Search time 184 Seconds
(without alignments)
47.759 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREBEKPF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003s.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	20	8 ADS13770	Adsl3770 Human Ang
2	106	100.0	20	8 ADS13769	Adsl3769 Human Ang
3	106	100.0	26	8 ADS13805	Adsl3805 Ang-1 lin
4	106	100.0	235	6 AAE32344	Aae32344 Human ang
5	106	100.0	261	8 ADI23636	Adi23636 Human Ang
6	106	100.0	298	8 ADI23638	Adi23638 Yeast GCN
7	106	100.0	310	8 ADI23640	Adi23640 Human CMP
8	106	100.0	312	8 ADI23642	Adi23642 Human COM
9	106	100.0	402	7 AAE38503	Aae38503 Human ang
10	106	100.0	402	9 AEA81248	Aea81248 Human ang
11	106	100.0	456	8 ADS13776	Adsl3776 Mouse Ang
12	106	100.0	456	8 ADS13775	Adsl3775 Human Ang
13	106	100.0	494	2 AAW47526	Aaw47526 Amino aci
14	106	100.0	498	2 AAR94603	Aar94603 Human TIE
15	106	100.0	498	2 AAW01409	Aaw01409 Human TIE
16	106	100.0	498	2 AAW47530	Aaw47530 Amino aci
17	106	100.0	498	2 AAW47528	Aaw47528 Amino aci
18	106	100.0	498	3 AAY78905	Aay78905 Human ang
19	106	100.0	498	3 AAY78902	Aay78902 Human ang
20	106	100.0	498	3 AAB28391	Aab28391 Human ang
21	106	100.0	498	5 AAU77943	Aau77943 Amino aci
22	106	100.0	498	6 ABP58063	Abp58063 Human ang
23	106	100.0	498	6 AAE32342	Aae32342 Human ang
24	106	100.0	498	7 AAE38487	Aae38487 Mouse ang

25	106	100.0	498	7 AAE38507	Aae38507 Human ang
26	106	100.0	498	7 AAE38501	Aae38501 Human ang
27	106	100.0	498	7 AAE38499	Aae38499 Mouse ang
28	106	100.0	498	7 AAE38486	Aae38486 Human ang
29	106	100.0	498	7 AAE38497	Aae38497 Mouse ang
30	106	100.0	498	7 ADD69265	Add69265 Human ang
31	106	100.0	498	7 ADP72296	Adp72296 Human ang
32	106	100.0	498	8 ADQ19778	Adq19778 Human sof
33	106	100.0	498	8 ADR87238	Adr87238 Amino aci
34	106	100.0	498	8 ADS13782	Adsl3782 Mouse ang
35	106	100.0	498	8 ADS13781	Adsl3781 Human ang
36	106	100.0	498	9 ADZ80187	Adz80187 Human TIE
37	106	100.0	498	9 AEA81247	Aea81247 Human ang
38	106	100.0	498	9 AEB87759	Aeb87759 Human Ang
39	96	90.6	495	3 AAY78907	Aay78907 Angiopole
40	96	90.6	495	3 AAY78904	Aay78904 Angiopole
41	96	90.6	495	3 AAB28393	Aab28393 Human ang
42	96	90.6	495	5 AAU77945	Aau77945 Amino aci
43	96	90.6	498	7 AAE38493	Aae38493 Pig angio
44	93	87.7	27	8 ADS13806	Adsl3806 Ang-1 lin
45	89.5	84.4	147	7 AAE38508	Aae38508 Human ang

ALIGNMENTS

RESULT 1
ADS13770
ID ADS13770 standard; peptide; 20 AA.
XX ADS13770;
XX
XX
DT 02-DEC-2004 (first entry)
XX
DE Human Ang-1 protein ECM-binding fragment.
XX
XX
KW Ang-1; extracellular matrix; ECM; angiotensin; vasotrophic;
KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;
KW gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004076650-A2.
XX
PD 10-SEP-2004.
XX
PF 27-FEB-2004; 2004WO-US006101.
XX
PR 27-FEB-2003; 2003US-0450582P.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Yu Q;
XX
DR WPI; 2004-653413/63.
DR N-PSDB; ADS13788.
XX
PT New pharmaceutical composition comprises a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or ischemia.
PT
PT
PS Claim 1; SEQ ID NO 2; 114pp; English.
XX
XX The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patients with the diseases

CC related to lack of blood vessels such as ischaemia in hearts and limbs;
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
 CC arteriosclerosis risk by maintaining the health and integrity of blood
 CC vessels; to assist the recovery of the patients who had stroke and the
 CC angioplasty procedure by promoting the growth/survival of endothelial
 CC cells and establish endothelial monolayer and inhibit excessive
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;
 CC to treat patients with restenosis by inhibiting re-closure of blood
 CC vessel after inserting stents into blood vessels; to make stable and
 CC functional artificial blood vessels comprising using the composition
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;
 CC of treating an individual suspected of having cancer; of preventing
 CC diabetes and/or arthritis in an individual suspected of being at risk of
 CC developing diabetes or arthritis. The pharmaceutical composition is
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
 CC angiogenesis, or arthritis. The present sequence represents an ECM-
 CC binding fragment of Ang-1 protein.
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 106; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.9e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20
 |||||
 DB 1 LCTKEGVLLKGGKREBEKPF 20

RESULT 2

ADSL3769

ID ADSL3769 standard; peptide; 20 AA.

XX ADSL3769;
 DT 02-DEC-2004 (first entry)
 XX Human Ang-1 protein ECM-binding fragment.

XX Ang-1; extracellular matrix; ECM; angiotensin; cytostatic; vasotropic;
 KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;
 KW gene therapy; human.

XX Homo sapiens.

XX WO2004076650-A2.

XX 10-SEP-2004.

XX 27-FEB-2004; 2004WO-US006101.

XX 27-FEB-2003; 2003US-0450582P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Yu Q;

XX WPI; 2004-653413/63.

DR N-PSDB; ADSL3787.

XX New pharmaceutical composition comprises a pharmaceutical carrier and an
 FT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein
 FT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
 PT ischemia.

XX Claim 1; SEQ ID NO 1; 114pp; English.

XX The invention relates to a pharmaceutical composition comprising a
 CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-
 CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also
 CC provided are methods of treating an individual suspected of having
 CC coronary artery disease, vascular disease or a condition involving

CC ischaemia; of promoting angiogenesis, endothelial survival and
 CC maintaining vascular integrity in an individual; of treating an
 CC individual suspected of having a disease related to lack of blood vessels
 CC to effectively promote angiogenesis in the patients with the diseases
 CC related to lack of blood vessels such as ischaemia in hearts and limbs;
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
 CC arteriosclerosis risk by maintaining the health and integrity of blood
 CC vessels; to assist the recovery of the patients who had stroke and the
 CC angioplasty procedure by promoting the growth/survival of endothelial
 CC cells and establish endothelial monolayer and inhibit excessive
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;
 CC to treat patients with restenosis by inhibiting re-closure of blood
 CC vessel after inserting stents into blood vessels; to make stable and
 CC functional artificial blood vessels comprising using the composition
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;
 CC of treating an individual suspected of having cancer; of preventing
 CC diabetes and/or arthritis in an individual suspected of being at risk of
 CC developing diabetes or arthritis. The pharmaceutical composition is
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
 CC angiogenesis, or arthritis. The present sequence represents an ECM-
 CC binding fragment of Ang-1 protein.
 XX

SQ Sequence 20 AA;

Query Match 100.0%; Score 106; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.9e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20
 |||||
 DB 1 LCTKEGVLLKGGKREBEKPF 20

RESULT 3

ADSL3805

ID ADSL3805 standard; peptide; 26 AA.

XX ADSL3805;

XX 02-DEC-2004 (first entry)

XX Ang-1 linker peptide region.

XX Ang-1; extracellular matrix; ECM; angiotensin; cytostatic; vasotropic;
 KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;
 KW gene therapy.

XX Homo sapiens.

XX WO2004076650-A2.

XX 10-SEP-2004.

XX 27-FEB-2004; 2004WO-US006101.

XX 27-FEB-2003; 2003US-0450582P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Yu Q;

XX WPI; 2004-653413/63.

XX New pharmaceutical composition comprises a pharmaceutical carrier and an
 FT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein
 FT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
 PT ischemia.

XX Example 1; Page 27; 114pp; English.

XX The invention relates to a pharmaceutical composition comprising a
 CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-

CC binding fragment of angiopoietin (Ang)-1 protein or a mutant Ang-1. Also
 CC provided are methods of treating an individual suspected of having
 CC coronary artery disease, vascular disease or a condition involving
 CC ischaemia; of promoting angiogenesis, endothelial survival and
 CC maintaining vascular integrity in an individual; of treating an
 CC individual suspected of having a disease related to lack of blood vessels
 CC to effectively promote angiogenesis in the patients with the diseases
 CC related to lack of blood vessels such as ischaemia in hearts and limbs;
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
 CC atherosclerosis, risk by maintaining the health and integrity of blood
 CC vessels; to assist the recovery of the patients who had stroke and the
 CC angioplasty procedure by promoting the growth/survival of endothelial
 CC cells and establish endothelial monolayer and inhibit excessive
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;
 CC to treat patients with restenosis by inhibiting re-closure of blood
 CC vessel after inserting stents into blood vessels; to make stable and
 CC functional artificial blood vessels comprising using the composition
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;
 CC of treating an individual suspected of having cancer; of preventing
 CC diabetes and/or arthritis in an individual suspected of being at risk of
 CC developing diabetes or arthritis. The pharmaceutical composition is
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
 CC angiogenesis, or arthritis. The present sequence represents a linker
 CC peptide region of Ang-1 protein.

XX SQ Sequence 26 AA;

Query Match 100.0%; Score 106; DB 8; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20
 |||||
 Db 7 LCTKEGVLKGGKREKEKPF 26

RESULT 4
 AAE32344

ID AAE32344 standard; protein; 235 AA.

XX AAE32344;

DT 24-MAR-2003 (first entry)

XX Human angiopoietin-1 (Ang-1) truncated protein #1.

XX Vascular endothelial growth factor; VEGF; angiogenesis; wound healing;
 KW bone growth; osteoporosis; osteoarthritis; bone reconstruction; ulcer;
 KW lesion; injury; trauma; periodontal condition; protein therapy; human;
 KW angiopoietin-1; Ang-1.

XX Homo sapiens.

XX WO200283851-A2.

XX 24-OCT-2002.

PF 10-APR-2002; 2002WO-US011406.

XX 10-APR-2001; 2001US-00832355.

XX (GENV-) GENVEC INC.

XX Kovesdi I, Kessler PD;

XX WPI; 2003-075536/07.

XX New fusion protein comprising a non-heparin-binding vascular endothelial
 PT growth factor (VEGF) peptide portion and a non-VEGF peptide portion,
 PT useful for promoting angiogenesis and/or bone growth in mammals.

XX Disclosure; Page 126-127; 191pp; English.

XX The invention relates to a fusion protein comprising non-heparin binding
 CC vascular endothelial growth factor (VEGF) peptide portion and a non-VEGF
 CC peptide portion useful for promoting angiogenesis and/or bone growth in
 CC mammalian host. The fusion protein is useful for promoting angiogenesis,
 CC wound healing and bone growth. Compositions containing bone growth
 CC promoting fusion protein can be used to treat osteoporosis, rheumatoid or
 CC osteoarthritis, to improve poor bone healing, to promote implant
 CC integration and function of artificial joints and to facilitate bone
 CC reconstruction. They can also be used to treat e.g. ulcers, lesions,
 CC injuries, burns, trauma, periodontal conditions, lacerations and other
 CC conditions. The invention is also useful in protein therapy. The present
 CC sequence is human angiopoietin-1 (Ang-1) truncated protein used in the
 CC invention

XX SQ Sequence 235 AA;

Query Match 100.0%; Score 106; DB 6; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20
 |||||
 Db 215 LCTKEGVLKGGKREKEKPF 234

RESULT 5

AD123636

ID AD123636 standard; protein; 261 AA.

XX AD123636;

XX 22-APR-2004 (first entry)

XX Human Ang-1 fibrinogen-like domain/Preprotrypsin signal.

XX Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;
 KW angiopoietin; coiled-coil domain; cell growth; proliferation;
 KW matrix protein; transcription factor; growth factor; secretory protein;
 KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;
 KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;
 KW endothelial precursor cell.

XX Homo sapiens.

XX Synthetic.

XX US2003220476-A1.

XX 27-NOV-2003.

XX 18-OCT-2002; 2002US-00273180.

XX 21-MAY-2002; 2002US-0382541P.

XX (KOHG/) KOH G Y.

XX Koh GY;

XX WPI; 2004-010889/01.

XX N-PSDB; AD123635.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked
 PT to either a receptor binding domain of ligand or ligand binding domain of
 PT a receptor, useful for inhibiting or promoting differential function.

XX Disclosure; SEQ ID NO 2; 38pp; English.

XX The invention relates to a coiled coil chimaeric molecule comprising a
 CC coiled-coil domain linked to either a receptor binding domain of a ligand
 CC or ligand binding domain of a receptor, which forms a biologically active
 CC multimer, and where the chimaeric molecule in its non-multimeric form is
 CC not biologically active. Also included are an isolated nucleic acid
 CC encoding the coiled coil chimaeric molecule, an expression vector

CC comprising the nucleic acid, a host cell comprising the vector, a soluble
 CC biologically active multimer comprising the coiled coil chimaeric
 CC molecule, promoting cell growth or proliferation, decreasing or
 CC inhibiting ligand activity or cell proliferation and making a chimaeric
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging
 CC to a matrix protein family, transcription factor family, growth factor
 CC family or secretory protein family. The coiled coil domain is from
 CC cartilage matrix protein (CMP) or cartilage oligomeric matrix protein
 CC (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The
 CC receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or
 CC inhibiting a differential function and/or influencing the phenotype, such
 CC as growth, survival, contractility, migration and/or proliferation of
 CC receptor-bearing cells such as endothelial cells, haematopoietic stem
 CC cells and endothelial precursor cells. The present sequence represents
 CC the fibrinogen-like domain of Ang-1 with a preprotrypsin leader.

XX Sequence 261 AA;

Query Match 100.0%; Score 106; DB 8; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.4e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20
 Db 139 LCTKEGVLLKGGKREBEKPF 158

RESULT 6
 ADI23638
 ID ADI23638 standard; protein; 298 AA.

XX AC ADI23638;

DT 22-APR-2004 (first entry)

XX Yeast GCN4 coiled-coil domain/Human Ang-1 cDNA.

XX Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;
 KW angiopoietin1; coiled-coil domain; cell growth; proliferation;
 KW matrix protein; transcription factor; growth factor; secretory protein;
 KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;
 KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;
 KW endothelial precursor cell; yeast.

XX Homo sapiens.

OS Saccharomyces cerevisiae.

OS Chimeric.

PN US2003220476-A1.

XX 27-NOV-2003.

PF 18-OCT-2002; 2002US-00273180.

XX 21-MAY-2002; 2002US-0382541P.

XX (KOHG/) KOH G Y.

XX Koh GY;

DR WPI; 2004-010889/01.

DR N-PSDB; ADI23637.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked
 PT to either a receptor binding domain of ligand or ligand binding domain of
 PT a receptor, useful for inhibiting or promoting differential function.

XX Example 5; SEQ ID NO 4; 38pp; English.

XX The invention relates to a coiled coil chimaeric molecule comprising a
 CC coiled-coil domain linked to either a receptor binding domain of a ligand
 CC or ligand binding domain of a receptor, which forms a biologically active

CC multimer, and where the chimaeric molecule in its non-multimeric form is
 CC not biologically active. Also included are an isolated nucleic acid
 CC encoding the coiled coil chimaeric molecule, an expression vector
 CC comprising the nucleic acid, a host cell comprising the vector, a soluble
 CC biologically active multimer comprising the coiled coil chimaeric
 CC molecule, promoting cell growth or proliferation, decreasing or
 CC inhibiting ligand activity or cell proliferation and making a chimaeric
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging
 CC to a matrix protein family, transcription factor family, growth factor
 CC family or secretory protein family. The coiled coil domain is from
 CC cartilage matrix protein (CMP) or cartilage oligomeric matrix protein
 CC (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The
 CC receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or
 CC inhibiting a differential function and/or influencing the phenotype, such
 CC as growth, survival, contractility, migration and/or proliferation of
 CC receptor-bearing cells such as endothelial cells, haematopoietic stem
 CC cells and endothelial precursor cells. The present sequence represents
 CC the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-
 CC coil domain.

XX Sequence 298 AA;

Query Match 100.0%; Score 106; DB 8; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20
 Db 64 LCTKEGVLLKGGKREBEKPF 83

RESULT 7
 ADI23640

ID ADI23640 standard; protein; 310 AA.

XX AC ADI23640;

DT 22-APR-2004 (first entry)

XX Human CMP coiled-coil domain/Ang-1.

XX Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;
 KW angiopoietin1; coiled-coil domain; cell growth; proliferation;
 KW matrix protein; transcription factor; growth factor; secretory protein;
 KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;
 KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;
 KW endothelial precursor cell.

XX Homo sapiens.

OS Synthetic.

XX US2003220476-A1.

XX 27-NOV-2003.

PF 18-OCT-2002; 2002US-00273180.

XX 21-MAY-2002; 2002US-0382541P.

XX (KOHG/) KOH G Y.

XX Koh GY;

XX WPI; 2004-010889/01.

DR N-PSDB; ADI23639.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked
 PT to either a receptor binding domain of ligand or ligand binding domain of
 PT a receptor, useful for inhibiting or promoting differential function.

XX Example 6; SEQ ID NO 6; 38pp; English.

CC The invention relates to a coiled coil chimaeric molecule comprising a
 CC coiled-coil domain linked to either a receptor binding domain of a ligand
 CC or ligand binding domain of a receptor, which forms a biologically active
 CC multimer, and where the chimaeric molecule in its non-multimeric form is
 CC not biologically active. Also included are an isolated nucleic acid
 CC encoding the coiled coil chimaeric molecule, an expression vector
 CC comprising the nucleic acid, a host cell comprising the vector, a soluble
 CC biologically active multimer comprising the coiled coil chimaeric
 CC molecule, promoting cell growth or proliferation, decreasing or
 CC inhibiting ligand activity or cell proliferation and making a chimaeric
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging
 CC to a matrix protein family, transcription factor family, growth factor
 CC family or secretory protein family. The coiled coil domain is from
 CC cartilage matrix protein (CMP) or cartilage oligomeric matrix protein
 CC (COMP). The receptor-binding domain binds to Tie2 or Tiel receptor. The
 CC receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or
 CC inhibiting a differential function and/or influencing the phenotype of
 CC as growth, survival, contractility, migration and/or proliferation of
 CC receptor-bearing cells such as endothelial cells, haematopoietic stem
 CC cells and endothelial precursor cells. The present sequence represents
 CC the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-
 CC coil domain.

XX SQ Sequence 310 AA;

Query Match 100.0%; Score 106; DB 8; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLGGKREBEKPF 20
 |||||
 Db 76 LCTKEGVLLGGKREBEKPF 95

RESULT 8
 ADI23642
 ID ADI23642 standard; protein; 312 AA.

AC ADI23642;
 XX
 DT 22-APR-2004 (first entry)
 XX Human COMP coiled-coil domain/Ang-1.
 XX
 DE Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;
 KW angiopoietin1; coiled-coil domain; cell growth; proliferation;
 KW matrix protein; transcription factor; growth factor; secretory protein;
 KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;
 KW Tie2 receptor; Tiel receptor; endothelial cell; haematopoietic stem cell;
 KW endothelial precursor cell.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2003220476-A1.
 XX
 XX 27-NOV-2003.
 XX
 XX 18-OCT-2002; 2002US-00273180.
 XX
 XX 21-MAY-2002; 2002US-0382541P.
 XX (KOHG/) KOH G Y.
 XX
 XX Koh GY;
 XX
 XX WPI; 2004-010889/01.
 XX N-PSDB; ADI23641.
 XX
 XX New coiled coil chimeric molecule comprising a coiled-coil domain linked
 PT to either a receptor binding domain of ligand or ligand binding domain of
 PT a receptor, useful for inhibiting or promoting differential function.

XX Example 7; SEQ ID NO 8; 38pp; English.

XX The invention relates to a coiled coil chimaeric molecule comprising a
 CC coiled-coil domain linked to either a receptor binding domain of a ligand
 CC or ligand binding domain of a receptor, which forms a biologically active
 CC multimer, and where the chimaeric molecule in its non-multimeric form is
 CC not biologically active. Also included are an isolated nucleic acid
 CC encoding the coiled coil chimaeric molecule, an expression vector
 CC comprising the nucleic acid, a host cell comprising the vector, a soluble
 CC biologically active multimer comprising the coiled coil chimaeric
 CC molecule, promoting cell growth or proliferation, decreasing or
 CC inhibiting ligand activity or cell proliferation and making a chimaeric
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging
 CC to a matrix protein family, transcription factor family, growth factor
 CC family or secretory protein family. The coiled coil domain is from
 CC cartilage matrix protein (CMP) or cartilage oligomeric matrix protein
 CC (COMP). The receptor-binding domain binds to Tie2 or Tiel receptor. The
 CC receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or
 CC inhibiting a differential function and/or influencing the phenotype of
 CC as growth, survival, contractility, migration and/or proliferation of
 CC receptor-bearing cells such as endothelial cells, haematopoietic stem
 CC cells and endothelial precursor cells. The present sequence represents
 CC the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-
 CC coil domain.

XX SQ Sequence 312 AA;

Query Match 100.0%; Score 106; DB 8; Length 312;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLGGKREBEKPF 20
 |||||
 Db 78 LCTKEGVLLGGKREBEKPF 97

RESULT 9
 AAE38503

ID AAE38503 standard; protein; 402 AA.

XX AAE38503;

AC AAE38503;
 XX
 DT 20-NOV-2003 (first entry)

XX Human angiopoietin-1 #4.

XX Angiopoietin-1; endothelium; cell proliferation; tumour; gene therapy;
 KW human.

XX Homo sapiens.

OS WO2003068165-A2.

PN 21-AUG-2003.

XX 14-FEB-2003; 2003WO-US004595.

XX 14-FEB-2002; 2002US-0356809P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Ellis LM;

XX WPI; 2003-697465/66.

XX Stabilizing the endothelium or reducing endothelial cell proliferation
 PT associated with a tumor comprises administering to a patient having a
 PT tumor angiopoietin-1 polypeptide.

XX Disclosure; Page 139-140; 157pp; English.

XX

Query Match 100.0%; Score 106; DB 8; Length 456;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
 |||||
 DB 222 LCTKEGVLKGGKREBEKPF 241

RESULT 12
 ADS13775
 ID ADS13775 standard; protein; 456 AA.
 XX
 AC ADS13775;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human Ang-1 protein non-ECM-binding fragment.
 XX
 KW Ang-1; extracellular matrix; ECM; angiotensin; cytotactic; vasotropic;
 KW antidiabetic; antiarthritic; cerebroprotective; angiogenic;
 KW gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004076650-A2.
 XX
 PD 10-SEP-2004.
 XX
 PF 27-FEB-2004; 2004WO-US006101.
 XX
 PR 27-FEB-2003; 2003US-0450582P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Yu Q;
 XX
 DR WPI; 2004-653413/63.
 DR N-PSDB; ADS13793.
 XX
 PT New pharmaceutical composition comprises a pharmaceutical carrier and an
 PT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein
 PT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
 PT ischemia.
 XX
 PS Claim 5; SEQ ID NO 7; 114pp; English.
 XX
 CC The invention relates to a pharmaceutical composition comprising a
 CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-
 CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also
 CC provided are methods of treating an individual suspected of having
 CC coronary artery disease, vascular disease or a condition involving
 CC ischaemia; of promoting angiogenesis, endothelial survival and
 CC maintaining vascular integrity in an individual; of treating an
 CC individual suspected of having a disease related to lack of blood vessels
 CC to effectively promote angiogenesis in the patients with the diseases
 CC related to lack of blood vessels such as ischaemia in hearts and limbs;
 CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
 CC atherosclerosis risk by maintaining the health and integrity of blood
 CC vessels; to assist the recovery of the patients who had stroke and the
 CC angioplasty procedure by promoting the growth/survival of endothelial
 CC cells and establish endothelial monolayer and inhibit excessive
 CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;
 CC to treat patients with restenosis by inhibiting re-closure of blood
 CC vessel after inserting stents into blood vessels; to make stable and
 CC functional artificial blood vessels comprising using the composition
 CC above; of identifying compounds that modulates binding of Ang-1 to ECM;
 CC of treating an individual suspected of having cancer; of preventing
 CC diabetes and/or arthritis in an individual suspected of being at risk of
 CC developing diabetes or arthritis. The pharmaceutical composition is
 CC useful for treating diseases and disorders, e.g. cancer, coronary artery
 CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
 CC angiogenesis, or arthritis. The present sequence represents a non-ECM-

CC binding fragment of Ang-1 protein.
 XX
 SQ Sequence 456 AA;
 Query Match 100.0%; Score 106; DB 8; Length 456;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
 |||||
 DB 222 LCTKEGVLKGGKREBEKPF 241

RESULT 13
 AAW47526
 ID AAW47526 standard; protein; 494 AA.
 XX
 AC AAW47526;
 XX
 DT 09-SEP-1998 (first entry)
 XX
 DE Amino acid sequence of chimeric TIE ligand 2N1C1F (chimera 4).
 XX
 KW Chimeric TIE ligand 2N1C1F; TIE-2 ligand; neovascularisation; tumour;
 KW human.
 XX
 OS Homo sapiens.
 XX
 PN WO9805779-A1.
 XX
 PD 12-FEB-1998.
 XX
 PF 01-AUG-1997; 97WO-US013557.
 XX
 PR 02-AUG-1996; 96US-0022999P.
 PR 25-OCT-1996; 96US-00740223.
 XX
 PA (REGE-) REGENERON PHARM INC.
 XX
 PI Davis S, Yancopoulos GD;
 XX
 DR WPI; 1998-145615/13.
 DR N-PSDB; AAV18613.
 XX
 PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound
 PT healing.
 XX
 PS Claim 20; Fig 27; 202pp; English.
 XX
 CC This is the amino acid sequence of the chimeric TIE ligand 2N1C1F, used
 CC in the method of the invention, involving the production of TIE-2 ligands
 CC which promote healing. The nucleic acids, vectors and host cells used in
 CC the method of the invention are useful for the recombinant production of
 CC the ligands. The ligands, etc. are useful for blocking blood vessel
 CC growth, promoting neovascularisation, promoting the growth or
 CC differentiation of a cell expressing the TIE receptor, blocking the
 CC growth or differentiation of a cell expressing the TIE receptor and for
 CC attenuating or preventing tumour growth in a human
 XX
 SQ Sequence 494 AA;
 Query Match 100.0%; Score 106; DB 2; Length 494;
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREBEKPF 20
 |||||
 DB 260 LCTKEGVLKGGKREBEKPF 279

RESULT 14
 AAR94603
 ID AAR94603 standard; protein; 498 AA.

```

XX AAR94603;
AC
XX 28-OCT-1996 (first entry)
DT
XX Human TIE-2 ligand 1 derived from lambda-gt10 clone.
XX
XX Angiogenesis; neovascularisation; tumour development; wound healing; TIE;
XX tyrosine kinase with Ig and EGF homology domains; vector; recombinant;
XX clone; diagnosis; ischaemia; thromboembolytic disease; atherosclerosis;
XX inflammation; diabetes; ligand bodies; delivery; targeting.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 269
XX /note= "extra Gly residue not present in TIE-2 ligand 1
XX derived from T98G clone (see AAT14649 and AAR94604)"
XX
XX WO9611269-A2.
XX
XX 18-APR-1996.
XX
XX 06-OCT-1995; 95WO-US012935.
XX
XX 07-OCT-1994; 94US-00319932.
XX
XX 27-OCT-1994; 94US-00320261.
XX
XX 02-DEC-1994; 94US-00348492.
XX
XX 09-DEC-1994; 94US-00353503.
XX
XX 17-JAN-1995; 95US-00373579.
XX
XX 06-APR-1995; 95US-00418595.
XX
XX (REG-) REGENERON PHARM INC.
XX
XX Davis S, Bruno J, Goldfarb M, Aldrich TH, Maisompierre PC;
XX Radziejewski C, Jones PF, Yancopoulos GD;
XX WPI; 1996-209850/21.
XX N-PSDB; AAT14648.
XX
XX Nucleic acid encoding TIE-2 ligand and related vectors - useful in
XX diagnosis and treatment of neovascularisation, tumours, etc., or to
XX promote wound healing, etc.
XX
XX Claim 2; Fig 4; 84pp; English.
XX
XX AAR94603 is a recombinant human TIE-2 (HTIE-2) ligand 1 derived from a
XX lambda-gt10 clone. The ligand has an extra Gly residue (aa 269) as
XX compared to the hTIE-2 ligand from a T98G clone (see AAT14649 and
XX AAR94604). hTIE-2 ligand DNAs of the invention are recombinant versions
XX of the native ligand coding sequences and may be used to produce the
XX ligands at a high yield. Antibodies and receptor bodies that bind to TIE-
XX 2 ligands may be used to inhibit angiogenesis and neovascularisation
XX (e.g. associated with tumour development) and the TIE-2 ligands
XX themselves are useful to promote neovascularisation and wound healing
XX e.g. for treatment of ischaemia. TIE-2 ligands are also useful to treat
XX thromboembolytic disease, atherosclerosis, inflammation and diabetes.
XX Ligand bodies contg. TIE-2 ligands may also be useful for the delivery
XX and targeting of growth factors, toxins etc. to sites where their
XX presence is advantageous
XX
XX Sequence 498 AA;
XX
XX Query Match 100.0%; Score 106; DB 2; Length 498;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-08;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LCTKEGVLKGGKREKPPF 20
XX ||||||||||||||||
XX 264 LCTKEGVLKGGKREKPPF 283
XX
XX RESULT 15

```

```

AAW01409
ID AAW01409 standard; protein; 498 AA.
XX
XX AAW01409;
AC
XX 11-FEB-1997 (first entry)
DT
XX Human TIE-2 ligand 1 (lambda-gt10 clone product).
XX
XX TIE-2 ligand 1; tyrosine kinase with Ig and EGF homology domain;
XX receptor; agonist; neovascularisation; wound healing; ischaemia;
XX leukaemia; thrombocytopaenia; anaemia; angiogenesis; tumour;
XX atherosclerosis; inflammation; diagnosis; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 269
XX /note= "Gly-269 is absent in TIE-2 ligand 1 from
XX glioblastoma T98G"
XX
XX WO9631598-A1.
XX
XX 10-OCT-1996.
XX
XX 05-APR-1996; 96WO-US004806.
XX
XX 06-APR-1995; 95US-00418595.
XX
XX 06-OCT-1995; 95WO-US012935.
XX
XX (REG-) REGENERON PHARM INC.
XX
XX Davis S, Bruno J, Goldfarb M, Aldrich TH, Maisompierre PC;
XX Radziejewski C, Jones PF, Yancopoulos GD;
XX WPI; 1996-465021/46.
XX N-PSDB; AAT44319.
XX
XX TIE-2 agonists and antagonists and related DNA - useful for promoting or
XX blocking neovascularisation, etc.
XX
XX Claim 14; Fig 4; 113pp; English.
XX
XX Human TIE-2 (tyrosine kinase with Ig and EGF homology domains) ligand 1
XX (AAW01409) is a ligand that binds the TIE-2 receptor. Its amino acid
XX sequence was deduced from a cDNA clone (AAT44319) derived from foetal
XX lung cells. A variant form of the ligand (AAW01410), lacking Gly-269, is
XX produced by a cDNA clone (AAT44320) from glioblastoma T98G cells. Both
XX ligands are TIE-2 agonists useful in promoting the growth, survival,
XX migration and/or differentiation and/or stabilisation or destabilisation
XX of cells expressing the TIE-2 receptor. They can be isolated from natural
XX sources or produced in transformed host cells
XX
XX Sequence 498 AA;
XX
XX Query Match 100.0%; Score 106; DB 2; Length 498;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-08;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LCTKEGVLKGGKREKPPF 20
XX ||||||||||||||||
XX 264 LCTKEGVLKGGKREKPPF 283
XX

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Search completed: December 29, 2005, 15:36:17
Job time : 186 secs

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OM protein - protein search, using sw model

Run on: December 29, 2005, 15:32:59 ; Search time 46 Seconds
(without alignments)
35.946 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKRGVLLKGRKEEKP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pap.*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pap.*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pap.*

4: /cgn2_6/ptodata/1/iaa/PCITUS_COMB.pap.*

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6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	100.0	478	2	US-08-740-223A-7
2	106	100.0	478	2	US-09-709-188-7
3	106	100.0	478	2	US-10-225-060-7
4	106	100.0	495	2	US-08-740-223A-26
5	106	100.0	495	2	US-09-709-188-26
6	106	100.0	495	2	US-10-225-060-26
7	106	100.0	497	2	US-08-740-223A-14
8	106	100.0	497	2	US-09-709-188-14
9	106	100.0	497	2	US-10-225-060-14
10	106	100.0	498	1	US-08-373-579-2
11	106	100.0	498	1	US-08-418-595-2
12	106	100.0	498	1	US-08-665-926-2
13	106	100.0	498	1	US-08-348-452-2
14	106	100.0	498	2	US-09-162-437-2
15	106	100.0	498	2	US-08-740-223A-2
16	106	100.0	498	2	US-08-740-223A-20
17	106	100.0	498	2	US-09-351-457-2
18	106	100.0	498	2	US-09-561-500-2
19	106	100.0	498	2	US-09-561-108-2
20	106	100.0	498	2	US-09-351-543-2
21	106	100.0	498	2	US-09-561-526-2
22	106	100.0	498	2	US-09-202-491-5
23	106	100.0	498	2	US-09-202-491-6
24	106	100.0	498	2	US-08-817-318-2
25	106	100.0	498	2	US-09-709-188-2
26	106	100.0	498	2	US-09-709-188-20
27	106	100.0	498	2	US-09-561-499-2

Sequence 2, Appli
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Sequence 2, Appli
Sequence 2, Appli
Sequence 20, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 6, Appli
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Sequence 6, Appli
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ALIGNMENTS

RESULT 1
US-08-740-223A-7
; Sequence 7, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; NUMBER OF INVENTION: Intercellular Signalling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740, 223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/022/999
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Mature T11 protein
; LOCATION: 1...478
; OTHER INFORMATION:
; US-08-740-223A-7

Query Match 100.0%; Score 106; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREERKPF 20
    |||||
Db 244 LCTKEGVLLKGGKREERKPF 263

RESULT 2
US-09-709-188-7
; Sequence 7, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-709-188-7

Query Match 100.0%; Score 106; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREERKPF 20
    |||||
Db 244 LCTKEGVLLKGGKREERKPF 263

RESULT 3
US-10-225-060-7
; Sequence 7, Application US/10225060
; Patent No. 6825008
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-060-7

Query Match 100.0%; Score 106; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREERKPF 20
    |||||
Db 244 LCTKEGVLLKGGKREERKPF 263

RESULT 4
US-08-740-223A-26
; Sequence 26, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 60/022/999
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 495 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: 2N1C1F (chimera 4)
; LOCATION: 1...495
; OTHER INFORMATION:
US-08-740-223A-26

Query Match 100.0%; Score 106; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREERKPF 20
    |||||
Db 261 LCTKEGVLLKGGKREERKPF 280

RESULT 5
US-09-709-188-26
; Sequence 26, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/09/709,188
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
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; Sequence 2, Application US/08665926
; Patent No. 5851797
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al.
; TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,926
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert J. Cobert
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-2113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-665-926-2

Query Match 100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLKGGKREBKPF 20
Db 264 LCTKEGVLKGGKREBKPF 283

RESULT 13
US-08-348-492-2
; Sequence 2, Application US/08348492
; Patent No. 5879672
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,492
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempner, Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 330B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 347-7000
; TELEFAX: (914) 347-2113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-348-492-2

Query Match 100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLKGGKREBKPF 20
Db 264 LCTKEGVLKGGKREBKPF 283

RESULT 14
US-09-162-437-2
; Sequence 2, Application US/09162437
; Patent No. 6166185
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/162,437
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/418,595
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,579
; FILING DATE: 17-JAN-1995
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.

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/ / REGISTRATION NUMBER: 36,108
/ / REFERENCE/DOCKET NUMBER: REG 330-D
/ /
/ / TELECOMMUNICATION INFORMATION:
/ /
/ / TELEPHONE: (914) 345-7400
/ / TELEFAX: (914) 345-7721
/ /
/ / INFORMATION FOR SEQ ID NO: 2:
/ / SEQUENCE CHARACTERISTICS:
/ / LENGTH: 498 amino acids
/ / TYPE: amino acid
/ / TOPOLOGY: linear
/ / MOLECULE TYPE: protein
/ /
/ / US-09-162-437-2

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Query Match      100.0%; Score 106; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20: Conservative 0; Mismatches 0; Indels
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Qy 1 LCTKEGVLLKGGKREEEKP 20
Db 264 LCTKEGVLLKGGKREEEKP 283

RESULT 15

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US-08/740-223A-2
/ Sequence 2, Application US/08740223A
/ Patent No. 6265564
/ GENERAL INFORMATION:
/ APPLICANT: Davis, et al.
/ TITLE OF INVENTION: Expressed Ligand - Vascular
/ TITLE OF INVENTION: Intercellular Signalling Molecule
/ NUMBER OF SEQUENCES: 28
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Regeneron Pharmaceuticals, Inc.
/ STREET: 777 Old Saw Mill Road
/ CITY: Tarrytown
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10591
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/740,223A
/ FILING DATE: 25-OCT-1996
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: USSN 60/022/999
/ FILING DATE: 02-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cobert, Robert J
/ REGISTRATION NUMBER: 36,108
/ REFERENCE/DOCKET NUMBER: REG 333
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 914-345-7400
/ TELEFAX: 914-345-7721
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 498 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ FEATURE:
/ NAME/KEY: Human TIE-2 ligand 1
/ LOCATION: 1...498
/ OTHER INFORMATION: from clone gt10 encoding htie-2
/ OTHER INFORMATION: ligand 1
US-08-740-223A-2

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Query Match 100.0%; Score 106; DB 2; Length 498;

Best Local Similarity	100.0%	Pred. No. 3.3e-09;	
Matches 20;	Conservative	0;	Mismatches 0;
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			Gaps 0;

Qy 1 LCTKEGVLLKGGKREEKPF 20
Db 264 LCTKEGVLLKGGKREEKPF 283

Search completed: December 29, 2005, 15:41:47
Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 15:36:24 ; Search time 160 Seconds
(without alignments)
52.229 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREEEKPF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	106	100.0	20	4	US-10-789-222-1
2	106	100.0	20	4	US-10-789-222-2
3	106	100.0	235	3	US-09-832-355A-18
4	106	100.0	260	4	US-10-273-180-2
5	106	100.0	298	4	US-10-273-180-4
6	106	100.0	309	4	US-10-273-180-6
7	106	100.0	312	4	US-10-273-180-8
8	106	100.0	402	4	US-10-367-259A-36
9	106	100.0	402	6	US-11-019-829-115
10	106	100.0	456	4	US-10-789-222-7
11	106	100.0	456	4	US-10-789-222-8
12	106	100.0	478	4	US-10-225-060-7
13	106	100.0	478	5	US-10-928-911-7
14	106	100.0	478	6	US-11-073-120-7
15	106	100.0	495	4	US-10-225-060-26
16	106	100.0	495	5	US-10-928-911-26
17	106	100.0	495	6	US-11-073-120-26
18	106	100.0	497	4	US-10-225-060-14
19	106	100.0	497	5	US-10-928-911-14
20	106	100.0	497	6	US-11-073-120-14
21	106	100.0	498	3	US-09-998-831-2
22	106	100.0	498	3	US-09-897-306-13
23	106	100.0	498	3	US-09-832-355A-15
24	106	100.0	498	3	US-09-998-833-2
25	106	100.0	498	4	US-10-179-744-2
26	106	100.0	498	4	US-10-186-817-2
27	106	100.0	498	4	US-10-215-224-5

28	106	100.0	498	4	US-10-215-224-6	Sequence 6, Appli
29	106	100.0	498	4	US-10-214-812-5	Sequence 5, Appli
30	106	100.0	498	4	US-10-214-812-6	Sequence 6, Appli
31	106	100.0	498	4	US-10-225-060-2	Sequence 2, Appli
32	106	100.0	498	4	US-10-225-060-20	Sequence 20, Appli
33	106	100.0	498	4	US-10-321-332-2	Sequence 2, Appli
34	106	100.0	498	4	US-10-136-819-12	Sequence 12, Appli
35	106	100.0	498	4	US-10-179-615-2	Sequence 2, Appli
36	106	100.0	498	4	US-10-179-820-2	Sequence 2, Appli
37	106	100.0	498	4	US-10-373-561-2	Sequence 2, Appli
38	106	100.0	498	4	US-10-367-259A-13	Sequence 13, Appli
39	106	100.0	498	4	US-10-367-259A-14	Sequence 14, Appli
40	106	100.0	498	4	US-10-367-259A-24	Sequence 24, Appli
41	106	100.0	498	4	US-10-367-259A-26	Sequence 26, Appli
42	106	100.0	498	4	US-10-367-259A-28	Sequence 28, Appli
43	106	100.0	498	4	US-10-367-259A-40	Sequence 40, Appli
44	106	100.0	498	4	US-10-789-222-13	Sequence 13, Appli
45	106	100.0	498	4	US-10-789-222-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1

US-10-789-222-1

; Sequence 1, Application US/10789222

; Publication No. US20040186054A1

; GENERAL INFORMATION:

; APPLICANT: Yu, Qin

; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses

; TITLE OF INVENTION: of the Same

; FILE REFERENCE: UPN0003-100 (P3115)

; CURRENT APPLICATION NUMBER: US/10/789, 222

; CURRENT FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: US 60/450,582

; PRIOR FILING DATE: 2003-02-27

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-789-222-1

Query Match 100.0%; Score 106; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.5e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREEEKPF 20

Db 1 LCTKEGVLLKGGKREEEKPF 20

RESULT 2

US-10-789-222-2

; Sequence 2, Application US/10789222

; Publication No. US20040186054A1

; GENERAL INFORMATION:

; APPLICANT: Yu, Qin

; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses

; TITLE OF INVENTION: of the Same

; FILE REFERENCE: UPN0003-100 (P3115)

; CURRENT APPLICATION NUMBER: US/10/789, 222

; CURRENT FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: US 60/450,582

; PRIOR FILING DATE: 2003-02-27

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 20

; TYPE: PRT

; ORGANISM: mouse

; US-10-789-222-2

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; CURRENT APPLICATION NUMBER: US/10/273,180
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-273-180-4

Query Match      100.0%; Score 106; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2,9e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREBEKPF 20
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Db 64 LCTKEGVLLKGGKREBEKPF 83

RESULT 6
US-10-273-180-6
; Sequence 6, Application US/10273180
; Publication No. US20030220476A1
; GENERAL INFORMATION:
; APPLICANT: KOH, Gou Young
; TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
; FILE REFERENCE: 10010-00001
; CURRENT APPLICATION NUMBER: US/10/273,180
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-273-180-6

Query Match      100.0%; Score 106; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREBEKPF 20
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Db 75 LCTKEGVLLKGGKREBEKPF 94

RESULT 7
US-10-273-180-8
; Sequence 8, Application US/10273180
; Publication No. US20030220476A1
; GENERAL INFORMATION:
; APPLICANT: KOH, Gou Young
; TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
; FILE REFERENCE: 10010-00001
; CURRENT APPLICATION NUMBER: US/10/273,180
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-273-180-8

Query Match      100.0%; Score 106; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREBEKPF 20
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Db 78 LCTKEGVLLKGGKREBEKPF 97

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RESULT 8
US-10-367-259A-36
; Sequence 36, Application US/10367259A
; Publication No. US20030220250A1
; GENERAL INFORMATION:
; APPLICANT: ELLIS, LEE M.
; TITLE OF INVENTION: ANGIOPOIETIN-1 IN THE TREATMENT OF DISEASE
; FILE REFERENCE: UTSC:6980S
; CURRENT APPLICATION NUMBER: US/10/367,259A
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,809
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-259A-36
Query Match 100.0%; Score 106; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLKGGKREBEKPF 20
Db 264 LCTKEGVLKGGKREBEKPF 283
RESULT 9
US-11-019-829-115
; Sequence 115, Application US/11019829
; Publication No. US20050136465A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
; FILE REFERENCE: 22304
; CURRENT APPLICATION NUMBER: US/11/019,829
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: angiotensin 1 variant 2
; LOCATION: (1)...(402)
; OTHER INFORMATION: LocusID: 284; NM_139290
US-11-019-829-115
Query Match 100.0%; Score 106; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLKGGKREBEKPF 20
Db 264 LCTKEGVLKGGKREBEKPF 283
RESULT 10
US-10-789-222-7
; Sequence 7, Application US/10789222
; Publication No. US20040186054A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Qin
; TITLE OF INVENTION: Angiotensin and Fragments, Mutants, and Analogs Thereof and Uses
; FILE REFERENCE: UPN0003-100 (P3115)
; CURRENT APPLICATION NUMBER: US/10/789,222
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/450,582
; PRIOR FILING DATE: 2003-02-27

; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-222-7
Query Match 100.0%; Score 106; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLKGGKREBEKPF 20
Db 222 LCTKEGVLKGGKREBEKPF 241
RESULT 11
US-10-789-222-8
; Sequence 8, Application US/10789222
; Publication No. US20040186054A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Qin
; TITLE OF INVENTION: Angiotensin and Fragments, Mutants, and Analogs Thereof and Uses
; FILE REFERENCE: UPN0003-100 (P3115)
; CURRENT APPLICATION NUMBER: US/10/789,222
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/450,582
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 456
; TYPE: PRT
; ORGANISM: mouse
US-10-789-222-8
Query Match 100.0%; Score 106; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLKGGKREBEKPF 20
Db 222 LCTKEGVLKGGKREBEKPF 241
RESULT 12
US-10-225-060-7
; Sequence 7, Application US/10225060
; Publication No. US20030092891A1
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-060-7
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Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREEKPF 20
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Db 244 LCTKEGVLLKGGKREEKPF 263

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 15:33:14 ; Search time 13 Seconds
(without alignments)
11.521 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKGVLLKGGKREKEPF 20

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Total number of hits satisfying chosen parameters: 57103

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB ID	Description
1	44	41.5	275	7	US-11-110-977-2
2	43	40.6	415	7	US-11-182-946-6
3	43	40.6	589	6	US-10-467-657-4826
4	42.5	40.1	163	6	US-10-793-626-2598
5	41	38.7	134	6	US-10-467-657-7860
6	41	38.7	394	6	US-10-467-657-7966
7	41	38.7	412	7	US-11-082-389-96
8	40	37.7	257	6	US-10-632-150-40
9	40	37.7	257	7	US-11-073-457-40
10	40	37.7	257	7	US-11-073-460-40
11	39	36.8	70	7	US-11-057-047-3
12	39	36.8	245	6	US-10-131-826A-280
13	39	36.8	739	7	US-11-057-047-2
14	39	36.8	761	7	US-11-057-047-6
15	39	36.8	764	7	US-11-057-047-1
16	39	36.8	798	6	US-10-821-234-1034
17	38	35.8	213	6	US-10-995-561-842
18	38	35.8	213	6	US-10-995-561-843
19	38	35.8	217	6	US-10-995-561-845
20	38	35.8	247	6	US-10-131-826A-284
21	38	35.8	483	6	US-10-467-657-2774
22	38	35.8	598	7	US-11-082-389-398
23	38	35.8	739	7	US-11-107-028-6
24	38	35.8	968	7	US-11-000-463-281
25	37	34.9	145	6	US-10-467-657-6506

ALIGNMENTS

RESULT 1
US-11-110-977-2
; Sequence 2, Application US/11110977
; Publication No. US20050260682A1
; GENERAL INFORMATION:
; APPLICANT: Charmley, Patrick R.
; APPLICANT: Smith, Ryan C.
; APPLICANT: Argonza-Barrett, Rhodora H.
; APPLICANT: Fitzgibbon, Matthew P.
; APPLICANT: Wang, Kai P.
; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
; FILE REFERENCE: CECH18764
; CURRENT APPLICATION NUMBER: US/11/110,977
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/112,645
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/280,514
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-110-977-2
Query Match 41.5%; Score 44; DB 7; Length 275;
Best Local Similarity 52.9%; Pred. No. 4.1;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 1 LCTKGVLLKGGKREE 17
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Db 254 LCSSEVGLLKNAREQE 270
RESULT 2
US-11-182-946-6
; Sequence 6, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18

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; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 415
; TYPE: PRP
; ORGANISM: Homo sapiens
; US-11-182-946-6

Query Match      40.6%; Score 43; DB 7; Length 415;
Best Local Similarity 52.6%; Pred. No. 9.1;
Matches 10; Conservative 0; Mismatches 9; Indels 9; Gaps 0;

Qy 1 LCTKEGVLLKGGKREBEK 19
Db 250 LCRKLGTLKRHPGEESP 268

RESULT 3
US-10-467-657-4826
; Sequence 4826, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4826
; LENGTH: 589
; TYPE: PRP
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-4826

Query Match      40.6%; Score 43; DB 6; Length 589;
Best Local Similarity 69.2%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 3; Indels 3; Gaps 0;

Qy 6 GVLLKGGKREBEK 18
Db 365 GVSLAGAKQBESEK 377

RESULT 4
US-10-793-626-2598
; Sequence 2598, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2598
; LENGTH: 163
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:

; PRIOR APPLICATION NUMBER: US/10/163,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 415
; TYPE: PRP
; ORGANISM: Homo sapiens
; US-11-182-946-6

Query Match      40.1%; Score 42.5; DB 6; Length 163;
Best Local Similarity 47.6%; Pred. No. 4.1;
Matches 10; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

Qy 1 LCTKEGVLLKGGKREBEK 18
Db 142 ICTKEDIKAKVGRSREAPK 162

RESULT 5
US-10-467-657-7860
; Sequence 7860, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7860
; LENGTH: 134
; TYPE: PRP
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-7860

Query Match      38.7%; Score 41; DB 6; Length 134;
Best Local Similarity 72.7%; Pred. No. 5.8;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GVLLKGGKREBEK 16
Db 16 GVLLRGTKRED 26

RESULT 6
US-10-467-657-7966
; Sequence 7966, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7966
; LENGTH: 394
; TYPE: PRP
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-7966

Query Match      38.7%; Score 41; DB 6; Length 394;
Best Local Similarity 72.7%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      6 GVLKGGKREE 16
      |||:|:|:|:|
Db      276 GVLKGGTKRED 286

RESULT 7
US-11-082-389-96
; Sequence 96, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberbauer, Gregor
; TITLE OF INVENTION: CORNYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ*ID NO 96
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-96

Query Match      38.7%; Score 41; DB 7; Length 412;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 KEGVLLKGGK 13
      |||:|:|:|:|
Db      67 KDGVLKGGGE 76

RESULT 8
US-10-632-150-40
; Sequence 40, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27

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; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-40

Query Match      37.7%; Score 40; DB 6; Length 257;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      2 CTKEGVLLKGGKREE 16
      |||:|:|:|:|
Db      53 CQOEGVLPEGGVEEE 67

RESULT 9
US-11-073-457-40
; Sequence 40, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFER
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-40

Query Match      37.7%; Score 40; DB 7; Length 257;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      2 CTKEGVLLKGGKREE 16
      |||:|:|:|:|
Db      53 CQOEGVLPEGGVEEE 67

RESULT 10
US-11-073-460-40
; Sequence 40, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFER
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40

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; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-40

Query Match 37.7%; Score 40; DB 7; Length 257;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 4; Mismatches 4; Indels 4; Gaps 0;

Qy 2 CTKEGVLLKGGKREE 16
| : : : : :
Db 53 CQOEGVLPEGGVREE 67

RESULT 11
US-11-057-047-3
; Sequence 3, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057.047
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-057-047-3

Query Match 36.8%; Score 39; DB 7; Length 70;
Best Local Similarity 63.6%; Pred. No. 6.1;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

Qy 2 CTKEGVLLKGG 12
| : : : : :
Db 7 CSLEGVEIKGG 17

RESULT 12
US-10-131-826A-280
; Sequence 280, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 280
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-280

Query Match 36.8%; Score 39; DB 6; Length 245;
Best Local Similarity 43.8%; Pred. No. 23;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 4 KEGVLLKGGKREKEP 19
| : : : : :
Db 175 KEGEIMKGNHVKNKP 190

RESULT 13
US-11-057-047-2
; Sequence 2, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; TITLE OF INVENTION: Methods Related Thereto
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057.047
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-057-047-2

Query Match 36.8%; Score 39; DB 7; Length 739;

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Best Local Similarity 63.6%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
Db 12 CSLEGEVEIKGG 22

RESULT 14
US-11-057-047-6
; Sequence 6, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-057-047-6

Query Match 36.8%; Score 39; DB 7; Length 761;
Best Local Similarity 63.6%; Pred. No. 76;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
Db 34 CSLEGEVEIKGG 44

RESULT 15
US-11-057-047-1
; Sequence 1, Application US/11057047
; Publication No. US20050260198A1
; GENERAL INFORMATION:
; APPLICANT: Holers, Vernon
; APPLICANT: Thurman, Joshua
; APPLICANT: Taube, Christian
; APPLICANT: Gelfand, Erwin
; APPLICANT: Gilkeson, Gary
; TITLE OF INVENTION: Inhibition of Factor B, The Alternative Complement Pathway and
; FILE REFERENCE: 2848-66
; CURRENT APPLICATION NUMBER: US/11/057,047
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,594
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/636,239
; PRIOR FILING DATE: 2004-12-14
; PRIOR APPLICATION NUMBER: US04/015040
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-11-057-047-1

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Query Match 36.8%; Score 39; DB 7; Length 764;
Best Local Similarity 63.6%; Pred. No. 76;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 CTKEGVLLKGG 12
Db 37 CSLEGEVEIKGG 47
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Job time : 14 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 15:30:06 ; Search time 37 Seconds
(without alignments)
52.009 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREKPF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	46.2	658	2 B86599	metal transport P-
2	49	46.2	658	2 D72026	metal transport p-
3	49	46.2	659	2 A81742	cation-transportin
4	49	46.2	659	2 B71479	probable metal tra
5	49	46.2	683	2 C81515	cation-transportin
6	47	44.3	673	2 AG3521	cation-transportin
7	47	44.3	927	1 JQ0948	A5 antigen precurs
8	46.5	43.9	591	1 SYHTPP	CTP synthase (SC 6
9	46	43.4	389	2 S01371	myosin heavy chain
10	45	42.5	168	2 JG0184	fibroblast growth
11	45	42.5	257	2 E71601	probable integrin
12	45	42.5	450	2 S15675	globulin-2 precurs
13	44	41.5	97	2 T29766	hypothetical prote
14	44	41.5	141	2 T48751	hypothetical prote
15	44	41.5	154	2 T20508	hypothetical prote
16	44	41.5	228	2 C81184	conserved hypotet
17	44	41.5	281	2 B81440	acetylglutamate ki
18	44	41.5	396	2 A48336	coat protein - Sou
19	44	41.5	406	1 A70015	probable NADH2 deh
20	44	41.5	486	2 S63384	hypothetical prote
21	43	40.6	216	2 A56861	peptidylprolyl iso
22	43	40.6	227	2 F90249	ribose 5-phosphate
23	43	40.6	394	2 H97825	elongation factor
24	43	40.6	394	2 C71672	translation elonga
25	43	40.6	416	2 H69436	5-enolpyruvylshiki
26	43	40.6	477	2 T52382	zinc finger protei
27	43	40.6	504	2 T10698	legumin-like prote
28	43	40.6	590	2 C81911	nitrate/nitrite se
29	43	40.6	590	2 B81104	nitrate/nitrite se

30	43	40.6	1792	2 T08878	supervillin P205 -
31	42.5	40.1	71	2 C82807	30S ribosomal prot
32	42.5	40.1	204	2 E64507	molybdopterin-guan
33	42.5	40.1	284	2 F71091	hypothetical prote
34	42	39.6	134	2 S39046	phosphoneuroprotei
35	42	39.6	137	2 I56498	phosphoneuroprotei
36	42	39.6	140	2 A49669	synuclein alpha -
37	42	39.6	149	2 B43959	synuclein, form 2
38	42	39.6	187	2 S10721	cathepsin D inhibi
39	42	39.6	188	1 XKPODC	cathepsin D inhibi
40	42	39.6	220	1 XKPOD	aspartic proteinase
41	42	39.6	220	2 S52656	cathepsin D inhibi
42	42	39.6	220	2 S24186	aspartic proteinase
43	42	39.6	221	2 T07411	proteinase inhibit
44	42	39.6	221	2 T07413	proteinase inhibit
45	42	39.6	221	2 JQ2246	22.5K cathepsin D

ALIGNMENTS

RESULT 1

B86599

metal transport P-type ATPase [imported] - Chlamydomophila pneumoniae (strain J138)

C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: B86599

R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise

Nucleic Acids Res. 28, 2311-2314, 2000

A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A;Reference number: A86491; MUID:20330349; PMID:10871362

A;Accession: B86599

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-658 <STO>

A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:BA000008; NID:g8979242; PFI

A;Experimental source: strain J138

C;Genetics:

A;Gene: zntA

C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding do

Query Match 46.2%; Score 49; DB 2; Length 658;

Best Local Similarity 81.8%; Pred. No. 16;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12

Db 331 CAKHGVLLKGG 341

RESULT 2

D72026

metal transport P-type ATPase - Chlamydomophila pneumoniae (strain CWL029)

C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: D72026

R;Kelman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: D72026

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-658 <ARN>

A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001363; NID

A;Experimental source: strain CWL029

C;Genetics:

A;Gene: zntA

C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding do

F;478-620/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 46.2%; Score 49; DB 2; Length 658;

Best Local Similarity 81.8%; Pred. No. 16;

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Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
   |||||
Db 331 CAKHGVLLKGG 341

RESULT 3
A81742
cation-transporting ATPase, E1-E2 family TC0100 [imported] - Chlamydia muridarum (strain
C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: A81742
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; MUID:20150255; PMID:10684935
A/Accession: A81742
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-659 <TET>
A/Cross-references: UNIPROT:Q9PLJ9; UNIPARC:UPI00000577C9; GB:AE002277; GB:AE002160; NID
A/Experimental source: strain Nigg (MoPn)
C/Genetics:
A/Gene: TC0100
C/Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
F/478-620/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 46.2%; Score 49; DB 2; Length 659;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
   |||||
Db 331 CAKHGVLLKGG 341

RESULT 4
B71479
probable metal transport p-type ATPase - Chlamydia trachomatis (serotype D, strain UW3/C
C/Species: Chlamydia trachomatis
C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C/Accession: B71479
R/Stephens, R.S.; Kalman, S.; Lammel, C.J.; Pan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A/Reference number: A71570; MUID:99000809; PMID:9784136
A/Accession: B71479
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-659 <ARN>
A/Cross-references: UNIPROT:O84732; UNIPARC:UPI000000D3395; GB:AE001343; GB:AE001273; NID
A/Experimental source: serotype D, strain UW-3/Cx
C/Genetics:
A/Gene: znfA
C/Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
F/64-400/Domain: ATPase transduction domain homology <ATT>
F/478-620/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 46.2%; Score 49; DB 2; Length 659;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
   |||||
Db 331 CAKHGVLLKGG 341

RESULT 5
C81515
cation-transporting ATPase, E1-E2 family CP1001 [imported] - Chlamydia pneumoniae (s
C/Species: Chlamydia pneumoniae, Chlamydia pneumoniae

```

```

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: C81515
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A/Reference number: A81500; MUID:20150255; PMID:10684935
A/Accession: C81515
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-683 <REA>
A/Cross-references: UNIPROT:Q9K1U0; UNIPARC:UPI000000CCCD4; GB:AE002257; GB:AE002161; NID
A/Experimental source: strain AR39, HL cells
C/Genetics:
A/Gene: CP1001
C/Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
F/503-645/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 46.2%; Score 49; DB 2; Length 683;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGG 12
   |||||
Db 356 CAKHGVLLKGG 366

RESULT 6
AG3521
cation-transporting p-type ATPase b (EC 3.6.1.1-) [imported] - Brucella melitensis (strain
C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C/Accession: AG3521
R/DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagijs, S.; O'Callaghan, D.; Leteser
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A/Reference number: AD3252; PMID:11756688
A/Accession: AG3521
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-673 <KUR>
A/Cross-references: UNIPROT:Q8YDS8; UNIPARC:UPI0000058350; GB:AE008918; PIDN:AAL53338.1;
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BMEI10097
A/Map position: II
C/Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
C/Keywords: hydrolase

Query Match 44.3%; Score 47; DB 2; Length 673;
Best Local Similarity 56.2%; Pred. No. 33;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREE 16
   :|||:
Db 337 VCARGVLFKGGKALE 352

RESULT 7
JQ0948
A5 antigen precursor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C/Accession: JH0466; JQ0948
R/Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
A/Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homologi
A/Reference number: JH0466; MUID:91337458; PMID:1908252
A/Accession: JH0466
A/Molecule type: mRNA
A/Residues: 1-927 <TAK>
A/Cross-references: UNIPARC:UPI00000171502; GB:D10467; GB:D01077; NID:g222962; PIDN:BA001

```


A;Experimental source: tadpole, brain
A;Note: this protein has motifs homologous to complement components C1r and C1s and to d
C;Comment: This protein is a neuronal cell surface molecule involved in the neuronal re
C;Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal h
C;Keywords: duplication; glycoprotein; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-927/Product: A5 antigen #status predicted <ASA>
F;27-138/Domain: C1r/C1s repeat homology <C1R1>
F;147-262/Domain: C1r/C1s repeat homology <C1R2>
F;274-424/Domain: discoidin I amino-terminal homology <DNI>
F;430-584/Domain: discoidin I amino-terminal homology <DN2>
F;646-812/Domain: MAM homology <MAM>
F;861-883/Domain: transmembrane #status predicted <TM>
F;150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.3%; Score 47; DB 1; Length 927;
Best Local Similarity 53.3%; Pred. No. 44;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 GVLLKGGKREEEKP 20
DB 498 GVIIQGGKHENKVF 512
|||||:|:|

RESULT 8
SYHUTP
N;Alternate names: CTP-synthetase; UTP-ammonia ligase
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
R;Accession: S12791
R;Yamauchi, M.; Yamauchi, N.; Meuth, M.
EMBO J. 9, 2095-2099, 1990
A;Title: Molecular cloning of the human CTP synthetase gene by functional complementatio
A;Reference number: S12791; MUID:90291972; PMID:2113467
A;Accession: S12791
A;Molecule type: mRNA
A;Residues: 1-591 <YAM>
A;Cross-references: UNIPROT:P17812; UNIPARC:UPI0000163BFD; GB:X52142; NID:g30292; PIDN:C
C;Comment: This enzyme is a glutamine amidotransferase that catalyzes the terminal react
C;Genetics:
A;Gene: GDB:CTPS
A;Cross-references: GDB:126729; OMIM:123860
A;Map position: lp34.3-1p34.1
C;Superfamily: CTP synthase
C;Keywords: ligase; pyrimidine nucleotide biosynthesis

Query Match 43.9%; Score 46.5; DB 1; Length 591;
Best Local Similarity 31.4%; Pred. No. 35;
Matches 11; Conservative 4; Mismatches 5; Indels 15; Gaps 1;

QY 1 LCTKEGVLLKGG-----KREEEKP 20
DB 361 LCSAHGLVPGFGVGTGKQIAIARWQKRP 395
|||||:|:|

RESULT 9
S01371
myosin heavy chain, cardiac and skeletal muscle - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 30-Sep-1989 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: S01371; S67907
R;Casimir, C.M.; Gates, P.B.; Ross-Macdonald, P.B.; Jackson, J.F.; Patient, R.K.; Brocke
J. Mol. Biol. 202, 287-296, 1988
A;Title: Structure and expression of a newt cardio-skeletal myosin gene. Implications fo
A;Reference number: S01371; MUID:89011957; PMID:2459393
A;Accession: S01371
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-171 <CAS>
A;Cross-references: UNIPROT:Q7LZ84; UNIPARC:UPI0000177608
A;Note: the sequence from fig. 7 is inconsistent with that from fig. 5 in having 64-Ile,
A;Accession: S67907

A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 36-389 <CAS2>
A;Cross-references: UNIPARC:UPI0000177609
A;Note: the sequence from fig. 7 is inconsistent with that from fig. 5 in having 64-Ile,
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP; cardiac muscle; coiled coil; heart; muscle contraction; skeletal muscle,
Query Match 43.4%; Score 46; DB 2; Length 389;
Best Local Similarity 44.4%; Pred. No. 28;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREEEK 18
DB 249 LMEAEQIAMKGGKKQEQK 266
|||||:|:|

RESULT 10
JG0184
fibroblast growth factor - human
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
R;Accession: JG0184
R;Kok, L.D.S.; Tsui, S.K.W.; Waye, M.; Liew, C.C.; Lee, C.Y.; Fung, K.P.
Biochem. Biophys. Res. Commun. 255, 717-721, 1999
A;Title: Cloning and characterization of a cDNA encoding a novel fibroblast growth factor
A;Reference number: JG0184; MUID:99160419; PMID:10049777
A;Accession: JG0184
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-168 <KOK>
A;Cross-references: UNIPROT:P61328; UNIPARC:UPI0000040663; GB:U76381
C;Superfamily: fibroblast growth factor

Query Match 42.5%; Score 45; DB 2; Length 168;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 KEGVLLKGGKREEEKP 19
DB 117 KEGQIMKGNVETKTP 132
|||||:|:|

RESULT 11
E71601
probable integral membrane protein PFB0995w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Accession: E71601
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: E71601
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-257 <GAR>
A;Cross-references: UNIPROT:Q9TY93; UNIPARC:UPI00000814CB; GB:AE001431; GB:AE001362; NID:
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0995w

Query Match 42.5%; Score 45; DB 2; Length 257;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 11; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 4 KEGVLLK-----GGKREEEKP 19
DB 11 KSGVLLKDKNTEBGRKKRQKP 32
|||||:|:|

RESULT 12

S15675
Globulin-2 precursor - maize
C/Species: Zea mays (maize)
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S15675
R/Mallace, N.H.; Kriz, A.L.
Plant Physiol. 95, 973-975, 1991
A/Title: Nucleotide sequence of a cDNA clone corresponding to the maize globulin-2 gene.
A/Reference number: S15675
A/Accession: S15675
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-450 <WAL>
A/Cross-references: UNIPROT:Q7M1Z8; UNIPARC:UPI0000177E41
C/Superfamily: vicilin

Query Match 42.5%; Score 45; DB 2; Length 450;
Best Local Similarity 68.8%; Pred. No. 45;
Matches 11; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

Qy . 4 KEG-----VLLKGGKRE 15
Db 95 KEGGVIVLLRGGKRE 110
||| |||:|||||
||| |||:|||||

RESULT 13
T29766
hypothetical protein ZC581.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T29766
R/Waterston, B.; Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, May 1997
A/Description: The sequence of C. elegans cosmid ZC581.
A/Reference number: Z20682
A/Accession: T29766
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-97 <WAT>
A/Cross-references: UNIPARC:UPI000017BCE4; EMBL:AF003134; PIDN:AAB54143.1; GSPDB:GN00019
A/Experimental source: strain Bristol N2; clone ZC581
C/Genetics:
A/Gene: CESP:ZC581.5
A/Map position: 1
A/Introns: 74/1

Query Match 41.5%; Score 44; DB 2; Length 97;
Best Local Similarity 53.8%; Pred. No. 15;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 EGVLLKGGKRE 17
Db 31 ERIIMKGGKNEED 43
|:|:|:|:|:|:|:
|:|:|:|:|:|:|:

RESULT 14
T48751
hypothetical protein 8D4.250 [imported] - Neurospora crassa
C/Species: Neurospora crassa
C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
C/Accession: T48751
R/Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, April 2000
A/Reference number: Z24541
A/Accession: T48751
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-141 <SCH>
A/Cross-references: UNIPARC:UPI0000179478; EMBL:AL353819; GSPDB:GN00112; NCSP:8D4.250
A/Experimental source: cosmid contig 8D4; strain 74
C/Genetics:
A/Gene: NCSP:8D4.250
A/Map position: 2

C/Superfamily: Neurospora crassa hypothetical protein 8D4.250

Query Match 41.5%; Score 44; DB 2; Length 141;
Best Local Similarity 64.3%; Pred. No. 21;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TKEGVLLKGGKRE 16
||| |||:|:|:|:
||| |||:|:|:|:

Db 74 TKNKLLSGKDDE 87
||| |||:|:|:|:
||| |||:|:|:|:

RESULT 15

T20508

hypothetical protein F02E9.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T20508

R/Gray, I.

submitted to the EMBL Data Library, November 1996

A/Reference number: Z19285

A/Accession: T20508

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-154 <WIL>

A/Cross-references: UNIPROT:O01314; UNIPARC:UPI0000074F96; EMBL:Z81494; PIDN:CAB04047.1;

A/Experimental source: clone F02E9

C/Genetics:

A/Gene: CESP:F02E9.1

A/Map position: 1

A/Introns: 29/2; 52/2; 80/3; 131/3

Query Match 41.5%; Score 44; DB 2; Length 154;

Best Local Similarity 60.0%; Pred. No. 23;

Matches 12; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 1 LCTKEG--VLLKGGKRE 18
||| |||:|:|:|:
||| |||:|:|:|:

Db 53 LDTKNGKFVLLKNSENEEK 72
||| |||:|:|:|:
||| |||:|:|:|:

Search completed: December 29, 2005, 15:40:56

Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 15:29:18 ; Search time 230 Seconds
(without alignments)
61.350 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREBEKPF 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	159	2	Q5YLW1_HUMAN
2	106	100.0	498	1	ANGP1_HUMAN
3	106	100.0	498	1	ANGP1_MOUSE
4	106	100.0	498	2	Q5HYA0_HUMAN
5	106	100.0	498	2	Q6NWX7_MOUSE
6	106	100.0	498	2	Q8C2K6_MOUSE
7	96	90.6	498	2	Q9BDY8_PIG
8	89.5	84.4	147	2	Q8N6P3_HUMAN
9	89.5	84.4	497	1	ANGP1_RAT
10	89.5	84.4	521	2	Q6A0F0_MOUSE
11	86.5	81.6	497	2	Q60FC1_CANFA
12	85.5	80.7	481	1	ANGP1_BOVIN
13	76	71.7	504	2	Q6GNY4_XENLA
14	59	55.7	383	2	Q9CUL6_MOUSE
15	55	51.9	178	2	Q4RN08_TETNG
16	54	50.9	1040	2	Q8H7M2_ORYSA
17	53	50.0	890	2	Q8B488_FLAU
18	52.5	49.5	591	2	Q5XHA8_XENLA
19	51	48.1	181	2	Q8I6J1_CIOXA
20	51	48.1	273	2	Q9CST2_MOUSE
21	51	48.1	566	2	Q7Y188_ORYSA
22	51	48.1	691	2	Q7Y017_ORYSA
23	51	48.1	940	2	Q7XDX7_ORYSA
24	51	48.1	974	2	Q6L423_ORYSA
25	51	48.1	982	2	Q7XWN4_ORYSA
26	51	48.1	1059	2	Q60E55_ORYSA
27	51	48.1	1109	2	Q5KQJ6_ORYSA
28	51	48.1	1177	2	Q75J33_ORYSA
29	51	48.1	1180	2	Q75HCL_ORYSA
30	51	48.1	1198	2	Q6L559_ORYSA
31	51	48.1	1198	2	Q94GS7_ORYSA

32 51 48.1 1224 2 Q84TW9_ORYSA Q84tw9 oryza sativ
33 51 48.1 1225 2 Q5TKC1_ORYSA Q5tkc1 oryza sativ
34 51 48.1 1229 2 Q6I578_ORYSA Q6i578 oryza sativ
35 51 48.1 1264 2 Q7XP54_ORYSA Q7xp54 oryza sativ
36 51 48.1 1264 2 Q8LSK0_MAIZE Q8lsk0 zea mays (m
37 51 48.1 1274 2 Q9FW32_ORYSA Q9fw32 oryza sativ
38 51 48.1 1277 2 Q53KA0_ORYSA Q53ka0 oryza sativ
39 51 48.1 1282 2 Q7XRW0_ORYSA Q7xrw0 oryza sativ
40 51 48.1 1289 2 Q60E18_ORYSA Q60e18 oryza sativ
41 51 48.1 1297 2 Q6L563_ORYSA Q6l563 oryza sativ
42 51 48.1 1297 2 Q7XP63_ORYSA Q7xe63 oryza sativ
43 51 48.1 1302 2 Q6L4G8_ORYSA Q6l4g8 oryza sativ
44 51 48.1 1302 2 Q6LSB9_ORYSA Q6lsb9 oryza sativ
45 51 48.1 1302 2 Q75J10_ORYSA Q75j10 oryza sativ

ALIGNMENTS

RESULT 1
Q5YLW1_HUMAN
ID Q5YLW1_HUMAN PRELIMINARY; PRT; 159 AA.
AC Q5YLW1_
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Angiopoietin-A.
GN Names=AngA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wang H., Zhang Y., Liang H.C., Zhang M., Sun D.H., Wang B.,
RA Zhang G.Z.;
RT "The Expression of Angiopoietin-A During Vascular Development.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055342; AAL59669.1; -; mRNA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
SQ SEQUENCE 159 AA; 18221 MW; F129DA56FB6AFC66 CRC64;
Query Match 100.0%; Score 106; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGKREBEKPF 20
|||||
Db 77 LCTKEGVLLKGGKREBEKPF 96

RESULT 2
ANGP1_HUMAN
ID ANGP1_HUMAN STANDARD; PRT; 498 AA.
AC Q15389;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1).
GN Name=ANGPT1; Synonyms=KIAA0003;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.
RC TISSUE=Petal lung;
RX MEDLINE=971134663; PubMed=8980223; DOI=10.1016/S0092-8674(00)81812-7;
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maisnier P.C.,

RA Yancopoulos G.D.;
 RT "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by
 RT secretion-trap expression cloning.";
 RL Cell 87:1161-1169(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.
 RA Nakatukasa M., Konai K., Shiozawa S.;
 RT "Human angiopoietin-1 mRNA variant form.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.
 RA Shan Z.X., Yu X.Y., Lin Q.Y., Fu Y.H., Tan H.H., Zheng M., Lin S.G.;
 RT "Human angiopoietin-1 mRNA variant forms.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Bone marrow;
 RX MEDLINE=96051387; PubMed=7584026;
 RA Nemura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayashi Y.,
 RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
 RT "Prediction of the coding sequences of unidentified human genes. I.
 RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
 RT analysis of randomly sampled cDNA clones from human immature myeloid
 RT cell line KG-1.";
 RL DNA Res. 1:27-35(1994).
 RN [5]
 RP SEQUENCE REVISION.
 RX MEDLINE=22158633; PubMed=12168954;
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual
 RL curation of 330 KIAA cDNA clones.";
 RL DNA Res. 9:99-106(2002).
 CC -1- FUNCTION: Binds and activates TIE2 receptor by inducing its
 CC tyrosine phosphorylation. Implicated in endothelial developmental
 CC processes later and distinct from that of VEGF. Appears to play a
 CC crucial role in mediating reciprocal interactions between the
 CC endothelium and surrounding matrix and mesenchyme. Mediates blood
 CC vessel maturation/stability. It may play an important role in the
 CC heart early development.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Glycosylated.
 CC -1- MISCELLANEOUS: It may have a potential therapeutic utility since
 CC it can be used for specifically targeting tumor vasculature or for
 CC promoting angiogenic processes in certain organs such as an
 CC ischemic heart.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; U83508; AAB50557.1; -; mRNA.
 DR EMBL; AB084454; BAB91325.1; -; mRNA.
 DR EMBL; AY121504; AAB81745.1; -; mRNA.
 DR EMBL; AY144360; AAB52271.1; -; mRNA.
 DR EMBL; D13628; BAA02793.2; ALT_INIT; mRNA.
 DR HSSP; P02671; 1FZD.
 DR Ensembl; ENSG00000154188; Homo sapiens.
 DR HGNC; HGNC:484; ANGPT1.
 DR H-InvDB; HIX000720; -.
 DR MIM; 601667; -.
 DR GO; GO:0005102; F:receptor binding; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN AG C-TERMINAL; 1.
 DR Angiogenesis; Coiled coil; Differentiation;
 KW Glycoprotein; Polymorphism; Signal.
 FT SIGNAL 1 15
 FT CHAIN 16 498 Angiopoietin-1.

FT DOMAIN 284 498 Fibrinogen C-terminal.
 FT COILED 81 119 Potential.
 FT COILED 153 261 Potential.
 FT CARBOHYD 92 92 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 154 154 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 243 243 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 295 295 N-linked (GlcNAc...) (Potential).
 FT DISULFID 286 315 By similarity.
 FT DISULFID 439 452 Missing (in cell line T98G; may be due to
 FT VARIANT 269 269 exon slippage).
 FT FTID=VAR 009940.
 SQ SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;
 Query Match 100.0%; Score 105; DB 1; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LCTKEGVLLKGGKREBEKPF 20
 DQ 264 LCTKEGVLLKGGKREBEKPF 283
 RESULT 3
 ID ANGPT1_MOUSE STANDARD; PRT; 498 AA.
 AC Q08538;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Angiopoietin-1 precursor (ANG-1).
 GN Name-Angpt1; Synonyms-Angpt;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97134663; PubMed=8980223; DOI=10.1016/S0092-8674(00)81812-7;
 RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
 RA Ryan T.E., Bruno J., Radziejewski C., Maisonnier P.C.,
 RA Yancopoulos G.D.;
 RT "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by
 RT secretion-trap expression cloning.";
 RL Cell 87:1161-1169(1996).
 CC -1- FUNCTION: Binds and activates TIE2 receptor by inducing its
 CC tyrosine phosphorylation. Implicated in endothelial developmental
 CC processes later and distinct from that of VEGF. Appears to play a
 CC crucial role in mediating reciprocal interactions between the
 CC endothelium and surrounding matrix and mesenchyme. Mediates blood
 CC vessel maturation/stability. It may play an important role in the
 CC heart early development.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DEVELOPMENTAL STAGE: Early in development, at E9 to E11, it is
 CC found most prominently in the heart myocardium surrounding the
 CC endocardium. Later, it becomes more widely distributed, most often
 CC in the mesenchyme surrounding developing vessels, in close
 CC association with endothelial cells.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; U83509; AAB50558.1; -; mRNA.
 DR HSSP; P02671; 1FZD.
 DR Ensembl; ENSMUSG00000022309; Mus musculus.
 DR MGI; MGI:108448; Angpt1.
 DR GO; GO:0005615; C:extracellular space; TAS.

DR GO: 0005172; F:vascular endothelial growth factor receptor. . . ; TAS.
 DR GO: 0007492; P:endoderm development; TAS.
 DR GO: 0007169; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.
 KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;
 KW Glycoprotein; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 498 Angiopoietin-1.
 FT DOMAIN 284 498 Fibrinogen C-terminal.
 FT COILED 81 119 Potential.
 FT COILED 153 261 Potential.
 FT CARBOHYD 92 92 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 122 122 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 154 154 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 243 243 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 295 295 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 286 315 By similarity.
 FT DISULFID 439 452 By similarity.
 SQ SEQUENCE 498 AA; 57505 MW; 285B4FDEC260D800 CRC64;
 Query Match 100.0%; Score 106; DB 1; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LCTKEGVLLKGGKREBEKPF 20
 DB 264 LCTKEGVLLKGGKREBEKPF 283
 RESULT 4
 QSHYAO HUMAN
 ID QSHYAO HUMAN PRELIMINARY; PRT; 498 AA.
 AC QSHYAO
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DEL Hypothetical protein DKFZp686L10222.
 GN Name=DKFZp686L10222;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP TISSUE=Small intestine;
 RG The German cDNA Consortium;
 RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Oeanger A., Fobo G.,
 RA Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX648814; CAI45984.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;
 Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LCTKEGVLLKGGKREBEKPF 20
 DB 264 LCTKEGVLLKGGKREBEKPF 283
 RESULT 5
 Q6NWV7 MOUSE
 ID Q6NWV7 MOUSE PRELIMINARY; PRT; 498 AA.
 AC Q6NWV7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Angiopoietin 1.
 GN Name=Angptl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wegner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RC NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Embryo;
 RA Director MGC Project;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC067410; AAH67410.1; -; mRNA.
 DR GO: 0005615; C:extracellular space; TAS.
 DR GO: 0005172; F:vascular endothelial growth factor receptor. . . ; TAS.
 DR GO: 0007492; P:endoderm development; TAS.
 DR GO: 0007169; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.
 SQ SEQUENCE 498 AA; 57519 MW; FC36F905A9E79074 CRC64;
 Query Match 100.0%; Score 106; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LCTKEGVLLKGGKREBEKPF 20
 DB 264 LCTKEGVLLKGGKREBEKPF 283
 RESULT 6
 Q8C2K6 MOUSE
 ID Q8C2K6 MOUSE PRELIMINARY; PRT; 498 AA.
 AC Q8C2K6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
 DE length enriched library, clone:E430016L03 product:angiopoietin, full
 DE insert sequence.
 GN Name=Angptl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]


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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins K.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Beasak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029406; AAH29406.1; -; mRNA.
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;
KW Glycoprotein; Signal.
SQ SEQUENCE 147 AA; 17314 MW; 68DFD40DE06FA37E CRC64;

Query Match 84.4%; Score 89.5; DB 1; Length 147;
Best Local Similarity 95.0%; Pred. No. 1.8e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 LCTKEGVLLKGGKREBEKPF 20
Db ||||| ||||| ||||| ||||| |||||
10 LCTKE-VLLKGGKREBEKPF 28

RESULT 9
ANGPL RAT
ID ANGPL RAT STANDARD; PRT; 497 AA.
AC Q35460; Q8K4Q4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1).
GN Name=Angptl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar; TISSUE=Placenta;
RX MEDLINE=22346496; PubMed=12458684; DOI=10.1023/A:1020921818105;
RA Iizasa H., Bae S.H., Asashima T., Kitano T., Matsunaga N.,
RA Terasaki T., Kang Y.S., Nakashima E.;
RT Augmented expression of the tight junction protein occludin in brain
RT endothelial cell line TR-BBB by rat angiotensin-1 expressed in
RT baculovirus-infected sf plus insect cells."
RL Pharm. Res. 19:1757-1760 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 91-200.
RC STRAIN=Sprague-Dawley; TISSUE=Placenta;
RX MEDLINE=98451564; PubMed=9776732;
RA Mandriota S.J., Pepper M.S.;

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RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
RT endothelial cells by cytokines and hypoxia.";
RL Circ. Res. 83:852-859 (1998).
CC -i- FUNCTION: Binds and activates TIE2 receptor by inducing its
CC tyrosine phosphorylation. Implicated in endothelial developmental
CC processes later and distinct from that of VEGF. Appears to play a
CC crucial role in mediating reciprocal interactions between the
CC endothelium and surrounding matrix and mesenchyme. Mediates blood
CC vessel maturation/stability. It may play an important role in the
CC heart early development.
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AB080023; BAC10290.1; -; mRNA.
CC EMBL; AF030376; AAC78246.1; -; mRNA.
CC HSSP; P02671; 1FZD.
CC Ensembl; ENSRNOG00000005854; Rattus norvegicus.
CC RGD; 628896; Angptl.
CC GO; GO:0005102; P:receptor binding; TAS.
CC GO; GO:0001525; P:angiogenesis; IEP.
CC GO; GO:0048014; P:Tie receptor signaling pathway; IDA.
CC InterPro; IPR002181; Fibrinogen_C.
CC Pfam; PF00147; Fibrinogen_C; 1.
CC SMART; SM00186; FBG; 1.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;
KW Glycoprotein; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 497 Angiopoietin-1.
FT DOMAIN 283 497 Fibrinogen C-terminal.
FT COILED 81 119 Potential.
FT COILED 153 261 Potential.
FT CARBOHYD 92 92 N-linked (GLNAC. . .) (Potential).
FT CARBOHYD 122 122 N-linked (GLNAC. . .) (Potential).
FT CARBOHYD 154 154 N-linked (GLNAC. . .) (Potential).
FT CARBOHYD 243 243 N-linked (GLNAC. . .) (Potential).
FT CARBOHYD 294 294 N-linked (GLNAC. . .) (Potential).
FT DISULFID 285 314 By similarity.
FT DISULFID 438 451 By similarity.
FT CONFLICT 98 98 Q -> E (in Ref. 2).
FT CONFLICT 172 172 E -> K (in Ref. 2).
FT CONFLICT 189 189 E -> K (in Ref. 2).
SQ SEQUENCE 497 AA; 57461 MW; 08E66ABEBF869AB CRC64;

Query Match 84.4%; Score 89.5; DB 1; Length 497;
Best Local Similarity 95.0%; Pred. No. 6e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 LCTKEGVLLKGGKREBEKPF 20
Db ||||| ||||| ||||| ||||| |||||
264 LCTKE-VLLKGGKREBEKPF 282

RESULT 10
Q6A0F0 MOUSE
ID Q6A0F0 MOUSE PRELIMINARY; PRT; 521 AA.
AC Q6A0F0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MKIAA0003 protein (fragment).
GN Name=Angptl; Synonyms=MKIAA0003;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Adult spleen;
RX PubMed=15368895;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Saito S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 11:205-218(2004).
DR EMBL; AK172868; BAD32146.1; -; mRNA.
DR MGI; MGI:108448; Angptl.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005172; F:vascular endothelial growth factor receptor. .; TAS.
DR GO; GO:0007492; P:endothelium development; TAS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
FT NON TER 1
SQ SEQUENCE 521 AA; 60103 MW; 8E7061F2A570EDFA CRC64;

Query Match 84.4%; Score 89.5; DB 2; Length 521;
Best Local Similarity 95.0%; Pred. No. 6.2e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LCTKEGVLLKGGKREKPF 20
| | | | | | | | | | | | | | | | | | | | | |
Db 288 LCTKE-VLLKGGKREKPF 306

RESULT 11
ID Q60FC1 CANFA PRELIMINARY; PRT; 497 AA.
AC Q60FC1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Angiopietin-1.
GN Name=Ang-1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kato Y., Asano K.;
RT "Canis familiaris Angiopietin-1 mRNA, complete cds.";
RL EMBL; AB192412; BAD54826.1; -; mRNA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 497 AA; 57415 MW; 061AFC2B03E8F081 CRC64;

Query Match 81.6%; Score 86.5; DB 2; Length 497;
Best Local Similarity 90.0%; Pred. No. 0.00017;
Matches 18; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LCTKEGVLLKGGKREKPF 20
| | | | | | | | | | | | | | | | | | | | | |
Db 264 LCTKE-VLLKGGKREKPF 282

RESULT 12
ID ANGPI_BOVIN STANDARD; PRT; 481 AA.

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AC DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Angiopietin-1 precursor (ANG-1) (Fragment).
GN Name=ANGPT1; Synonyms=ANG1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=99054348; PubMed=9840613;
RA Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
RT "Analysis of blood vessel maturation processes during cyclic ovarian
RT angiogenesis.";
RL Lab. Invest. 78:1385-1394(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 91-200.
RC TISSUE=Liver;
RX MEDLINE=98451564; PubMed=9776732;
RA Mandiata S.J., Pepper M.S.;
RT "Regulation of angiopietin-2 mRNA levels in bovine microvascular
RT endothelial cells by cytokines and hypoxia.";
RL Circ. Res. 83:852-859(1998).
CC -1- FUNCTION: Binds and activates TIE2 receptor by inducing its
CC tyrosine phosphorylation. Implicated in endothelial developmental
CC processes later and distinct from that of VEGF. Appears to play a
CC crucial role in mediating reciprocal interactions between the
CC endothelium and surrounding matrix and mesenchyme. Mediates blood
CC vessel maturation/stability. It may play an important role in the
CC heart early development (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: Found to be expressed throughout the ovarian
CC cycle.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF093573; AAC61872.1; -; mRNA.
CC EMBL; AF032923; AAC78245.1; -; mRNA.
CC HSP; Q9U8W8; IJCN9.
CC InterPro; IPR002181; Fibrinogen_C.
CC Pfam; PF00147; Fibrinogen_C; 1.
CC SMART; SM00186; FBG; 1.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
CC Angiogenesis; Coiled coil; Developmental protein; Differentiation;
CC Glycoprotein; Signal.
FT SIGNAL 1 15
FT CHAIN 16 >481
FT DOMAIN 283 >481 Fibrinogen C-terminal.
FT COILED 153 261 Potential.
FT CARBOHYD 92 92 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 154 154 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 243 243 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 294 294 N-linked (GlcNAc. .) (Potential).
FT DISULFID 285 314 By similarity.
FT DISULFID 438 451 By similarity.
FT NON TER 481
SQ SEQUENCE 481 AA; 55557 MW; 8EEC9ED84FC2BB50 CRC64;

Query Match 80.7%; Score 85.5; DB 1; Length 481;
Best Local Similarity 90.0%; Pred. No. 0.00024;
Matches 18; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 LCTKEGVLLKGGKREKPF 20

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Db 264 LCTKE-VLLKGGKREKEKPF 282
||||| ||||| ||||| ||||| |||||
RESULT 13
Q6GN4_XENLA PRELIMINARY; PRT; 504 AA.
ID Q6GN4;
AC Q6GN4;
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC80788 protein.
GN Names=MGC80788;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udén T.B., Tohiyuki S., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Valley D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.B., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
Initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073367; AAH73367.1; -; mRNA.
DR GO; GO:0007596; P-blood coagulation; IEA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C DOMAIN; 1.
SQ SEQUENCE 504 AA; 57794 MW; FA4F7D4174A7D390 CRC64;

Query Match 71.78; Score 76; DB 2; Length 504;
Best Local Similarity 70.09; Pred. No. 0.007;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKEKPF 20
||||| ||||| ||||| ||||| |||||
Db 270 LCSKEGTVKNVKEKPF 289
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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Tanaka S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multipillar sequencer.";
RN Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CS7BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshino K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK015498; BAB29870.2; -; mRNA.
DR Ensembl; ENSMUSG0000024280; Mus musculus.
DR MGI; MGI:1922184; Armcd4.
KM Hypothetical protein.
FT NON TER 383 383
SQ SEQUENCE 393 AA; 43608 MW; AA688BA4AACB01D CRC64;

Query Match 55.7%; Score 59; DB 2; Length 383;
Best Local Similarity 68.8%; Pred. No. 2.1;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CTKEGVLLKGGKREE 17
Db 262 CSTGEVFLNGKTEEE 277

RESULT 15
Q4RNQ8_TETNG
ID Q4RNQ8_TETNG PRELIMINARY; PRT; 178 AA.
AC Q4RNQ8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 2 SCAP15010, whole genome shotgun sequence.
GN ORFNames=GSTENG00031451001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OK NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,
RA Daesilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Bernardis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01015010; CAG09974.1; -; Genomic_DNA.
DR InterPro; IPR011700; bZIP_2.
DR InterPro; IPR004827; TF_bZIP.
DR Pfam; PF07716; bZIP_2; 1.
DR PROSITE; PS00217; bZIP; 1.
DR PROSITE; PS00036; bZIP_BASIC; 1.
KM DNA-binding; Nuclear protein.
SQ SEQUENCE 178 AA; 19157 MW; 832C61408C134DCF CRC64;
Query Match 51.9%; Score 55; DB 2; Length 178;
Best Local Similarity 55.6%; Pred. No. 4.1;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 2 CTKEGVLLKGGKREEKP 19
Db 4 CCEGVLTAGKDKTEKP 21
Search completed: December 29, 2005, 15:40:14
Job time : 233 secs

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; OTHER INFORMATION: 2NIC1F (chimera 4)
US-09-709-188-26

Query Match
Best Local Similarity 100.0%; Score 106; DB 2; Length 495;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20
Db 261 LCTKEGVLLKGGKREBEKPF 280

RESULT 6
US-10-225-060-26
; Sequence 26, Application US/10225060
; Patent No. 6825008
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; OTHER INFORMATION: 2NIC1F (chimera 4)
US-10-225-060-26

Query Match
Best Local Similarity 100.0%; Score 106; DB 2; Length 495;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20
Db 261 LCTKEGVLLKGGKREBEKPF 280

RESULT 7
US-08-740-223A-14
; Sequence 14, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; TITLE OF INVENTION: Intercellular Signalling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536

; OTHER INFORMATION: 2NIC1F (chimera 4)
US-09-709-188-26

Query Match
Best Local Similarity 100.0%; Score 106; DB 2; Length 497;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20
Db 263 LCTKEGVLLKGGKREBEKPF 282

RESULT 8
US-09-709-188-14
; Sequence 14, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/09/709,188
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Mus sp.
; OTHER INFORMATION:
; OTHER INFORMATION: mouse TIR-2 ligand 1
US-08-740-223A-14

Query Match
Best Local Similarity 100.0%; Score 106; DB 2; Length 497;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGGKREBEKPF 20
Db 263 LCTKEGVLLKGGKREBEKPF 282

RESULT 9
US-10-225-060-14
; Sequence 14, Application US/10225060
; Patent No. 6825008
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188

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;; PRIOR FILING DATE: 2000-11-09
;; PRIOR APPLICATION NUMBER: 08/740,223
;; PRIOR FILING DATE: 1996-10-25
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 14
;; LENGTH: 497
;; TYPE: PRT
;; ORGANISM: Mus sp.
US-10-225-060-14

Query Match 100.0%; Score 106; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKPF 20
|||
Db 263 LCTKEGVLKGGKREKPF 282

RESULT 10
US-08-373-579-2
; Sequence 2, Application US/08373579
; Patent No. 5650490
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,579
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-373-579-2

Query Match 100.0%; Score 106; DB 1; Length 498;

Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LCTKEGVLKGGKREKPF 20
|||
Db 264 LCTKEGVLKGGKREKPF 283
RESULT 11
US-08-418-595-2
; Sequence 2, Application US/08418595
; Patent No. 5814464
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,595
; FILING DATE: 06-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,579
; FILING DATE: 17-JAN-1995
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-418-595-2

Query Match 100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLKGGKREKPF 20
|||
Db 264 LCTKEGVLKGGKREKPF 283

RESULT 12
US-08-665-926-2